

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Hein, Mich B.  
Hiatt, Andrew C.  
Fitchen, John H.
- (ii) TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT
- (iii) NUMBER OF SEQUENCES: 113
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: SEED and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98104
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 09-JAN-1998  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 310098.401C1
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

05005318 010998

Gln	Glu	Asp	Glu	Arg	Ile	Val	Leu	Val	Asp	Asn	Lys	Cys	Lys	Cys	Ala
1				5					10					15	
Arg	Ile	Thr	Ser	Arg	Ile	Ile	Arg	Ser	Ser	Glu	Asp	Pro	Asn	Glu	Asp
			20					25					30		
Ile	Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile	Val	Pro	Leu	Asn	Asn	Arg	Glu
		35					40					45			
Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg	Thr	Arg	Pro	Val	Tyr	His
	50					55					60				
Leu	Ser	Asp	Leu	Cys	Lys	Lys	Cys	Asp	Pro	Thr	Glu	Val	Glu	Leu	Asp
65					70					75					80
Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	Asn	Ile	Cys	Asp	Glu	Asp	Ser
				85					90					95	
Ala	Thr	Glu	Thr	Cys	Tyr	Thr	Tyr	Asp	Arg	Asn	Lys	Cys	Tyr	Thr	Ala
			100					105					110		
Val	Val	Pro	Leu	Val	Tyr	Gly	Gly	Glu	Thr	Lys	Met	Val	Glu	Thr	Ala
		115					120					125			
Leu	Thr	Pro	Asp	Ala	Cys	Tyr	Pro	Asp							
	130					135									

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Gln	Asp	Glu	Asn	Glu	Arg	Ile	Val	Val	Asp	Asn	Lys	Cys	Lys	Cys	Ala
1				5					10					15	
Arg	Ile	Thr	Ser	Arg	Ile	Ile	Pro	Ser	Ala	Glu	Asp	Pro	Ser	Gln	Asp
			20					25					30		
Ile	Val	Glu	Arg	Asn	Val	Arg	Ile	Ile	Val	Pro	Leu	Asn	Ser	Arg	Glu
		35					40					45			
Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Met	Arg	Thr	Lys	Pro	Val	Tyr	His
	50					55					60				

Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu  
 65 70 75 80  
 Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala  
 85 90 95  
 Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Asn Arg Val  
 100 105 110  
 Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met Val Glu Thr Ala Leu Thr  
 115 120 125  
 Pro Asp Ser Cys Tyr Pro Asp  
 130 135

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Asp Glu Ala Thr Ile Leu Ala Asp Asn Lys Cys Met Cys Thr Arg  
 1 5 10 15  
 Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp Pro Asn Glu Asp Ile  
 20 25 30  
 Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu Asn Asn Arg Glu Asn  
 35 40 45  
 Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu  
 50 55 60  
 Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp  
 65 70 75 80  
 Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys Asn Glu Asp Asp Gly  
 85 90 95  
 Val Pro Glu Thr Cys Tyr Met Tyr Asp Arg Asn Lys Cys Tyr Thr Thr  
 100 105 110  
 Met Val Pro Leu Arg Tyr His Gly Glu Thr Lys Met Val Gln Ala Ala  
 115 120 125  
 Leu Thr Pro Asp Ser Cys Tyr Pro Asp

2003400000

135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Glu	Asp	Glu	Ser	Thr	Val	Leu	Val	Asp	Asn	Lys	Cys	Gln	Cys	Val	Arg
1				5					10					15	
Ile	Thr	Ser	Arg	Ile	Ile	Arg	Asp	Pro	Asp	Asn	Pro	Ser	Glu	Asp	Ile
			20					25					30		
Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile	Val	Pro	Leu	Asn	Thr	Arg	Glu	Asn
		35					40					45			
Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg	Thr	Glu	Pro	Lys	Tyr	Asn	Leu
	50					55					60				
Ala	Asn	Leu	Cys	Lys	Lys	Cys	Asp	Pro	Thr	Glu	Ile	Glu	Leu	Asp	Asn
65					70					75					80
Gln	Val	Phe	Thr	Ala	Ser	Gln	Ser	Asn	Ile	Cys	Pro	Asp	Asp	Asp	Tyr
				85					90					95	
Ser	Glu	Thr	Cys	Tyr	Thr	Tyr	Asp	Arg	Asn	Lys	Cys	Tyr	Thr	Thr	Leu
			100					105					110		
Val	Pro	Ile	Thr	His	Arg	Gly	Val	Thr	Arg	Met	Val	Lys	Ala	Thr	Leu
		115					120					125			
Thr	Pro	Asp	Ser	Cys	Tyr	Pro	Asp								
	130						135								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Glu	Gln	Glu	Tyr	Ile	Leu	Ala	Asn	Asn	Lys	Cys	Lys	Cys	Val	Lys	Ile	
1				5				10				15				
Ser	Ser	Arg	Phe	Val	Pro	Ser	Thr	Glu	Arg	Pro	Gly	Glu	Glu	Ile	Leu	
				20				25				30				
Glu	Arg	Asn	Ile	Gln	Ile	Thr	Ile	Pro	Thr	Ser	Ser	Arg	Met	Xaa	Ile	
				35				40				45				
Ser	Asp	Pro	Tyr	Ser	Pro	Leu	Arg	Thr	Gln	Pro	Val	Tyr	Asn	Leu	Trp	
				50				55				60				
Asp	Ile	Cys	Gln	Lys	Cys	Asp	Pro	Val	Gln	Leu	Glu	Ile	Gly	Gly	Ile	
65				70				75				80				
Pro	Val	Leu	Ala	Ser	Gln	Pro	Xaa	Xaa	Ser	Xaa	Pro	Asp	Asp	Glu	Cys	
				85				90				95				
Tyr	Thr	Thr	Glu	Val	Asn	Phe	Lys	Lys	Lys	Val	Pro	Leu	Thr	Pro	Asp	
				100				105				110				
Ser	Cys	Tyr	Glu	Tyr	Ser	Glu										
				115												

(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

Asn	Lys	Cys	Met	Cys	Thr	Arg	Val	Thr	Ala	Arg	Ile	Arg	Gly	Thr	Arg
1				5					10					15	
Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Tyr	Ile	Arg	Ile	Asn	Val
			20					25					30		
Pro	Leu	Lys	Asn	Arg	Gly	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg
		35					40					45			
Asn	Gln	Pro	Val	Tyr	His	Leu	Ser	Pro	Ser	Cys	Lys	Lys	Cys	Asp	Pro
	50					55					60				
Tyr	Glu	Asp	Gly	Val	Val	Thr	Ala	Thr	Glu	Thr	Asn	Ile	Cys	Tyr	Pro
65					70					75					80

Asp Gln Gly Val Pro Gln Ser Cys Arg Asp Tyr Cys Pro Glu Leu Asp  
85 90 95

Arg Asn Lys Cys Tyr Thr Val Leu Val Pro Pro Gly Tyr Thr Gly Glu  
100 105 110

Thr Lys Met Val Gln Asn Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAT CAG GAA GAT GAA CGT ATT GTT CTG GTT GAC AAC AAG TGC AAG TGT	48
Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys	
1 5 10 15	
GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC TCA GAG GAC CCA AAT GAA	96
Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu	
20 25 30	
GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC GTC CCA CTG AAT AAC CGG	144
Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg	
35 40 45	
GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG CGC ACA CGC TTC GTA TAC	192
Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr	
50 55 60	
CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG	240
His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu	
65 70 75 80	
GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC	288
Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp	
85 90 95	
AGC GCT ACA GAA ACC TGC AGC ACC TAC GAT AGG AAC AAA TGC TAC ACG	336
Ser Ala Thr Glu Thr Cys Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr	
100 105 110	

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GCC GTG GTT CCG CTC GTG TAT GGT GGA GAG ACA AAA ATG GTG GAA ACT 384  
 Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr  
           115                          120                          125

GCC CTT ACG CCC GAT GCA TGC TAT CCG GAC TGAATTC 421  
 Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp  
           130                          135

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAT CAG AAG TGC AAG TGT GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC 48  
 Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser  
       1                          5                          10                          15

TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC 96  
 Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile  
           20                          25                          30

GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG 144  
 Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu  
           35                          40                          45

CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG GAT GAG 192  
 Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Asp Glu  
           50                          55                          60

GAC AGC GCT ACA GAA ACC TGC TG 215  
 Asp Ser Ala Thr Glu Thr Cys  
       65                          70

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

00005348-0109998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAACGT AACATCCGTA 60  
 TCATCGTCCC ACTGAATAAC CGGGAGAATA TCTCAGATCC TACAAGTCCG TTGCGCACAC 120  
 GCTTCGTATA CCACCTGTCA 140

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCAGAAGT GCAAGTGTGC TCGTATTACT T 31

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAT CTG TGT AAG AAG GAT GAA GAT TCC GCT ACA GAA ACC TGC 42  
 Asp Leu Cys Lys Lys Asp Glu Asp Ser Ala Thr Glu Thr Cys  
           75                          80                          85

TG 44

(2) INFORMATION FOR SEQ ID NO:12:

0505316 040593



- (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCACCTACGA TAGGAACAAA TGCTACACGG CCGTG GTTCC GCTCGTGTAT GGTGGAGAGA 60

CAAAAATGGT GGAAACTGCC CTTACGCCCC ATGCATGCTA CCCTGACTG 109

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAC	AAC	AAG	TGC	AAG	TGT	GCT	CGT	ATT	ACT	TCT	AGA	ATC	ATC	CGT	AGC	48
Asp	Asn	Lys	Cys	Lys	Cys	Ala	Arg	Ile	Thr	Ser	Arg	Ile	Ile	Arg	Ser	
15					20					25					30	
TCA	GAG	GAC	CCA	AAT	GAA	GAT	ATA	GTC	GAA	CGT	AAC	ATC	CGT	ATC	ATC	96
Ser	Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile	
				35					40					45		
GTC	CCA	CTG	AAT	AAC	CGG	GAG	AAT	ATC	TCA	GAT	CCT	ACA	AGT	CCG	TTG	144
Val	Pro	Leu	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	
			50					55					60			
CGC	ACA	CGC	TTC	GTA	TAC	CAC	CTG	TCA	GAT	CTG	TGT	AAG	AAG	TGT	GAT	192
Arg	Thr	Arg	Phe	Val	Tyr	His	Leu	Ser	Asp	Leu	Cys	Lys	Lys	Cys	Asp	
		65					70					75				
CCA	ACA	GAG	GTA	GAG	CTG	GAC	AAT	CAG	ATA	GTC	ACT	GCG	ACT	CAA	AGC	240
Pro	Thr	Glu	Val	Glu	Leu	Asp	Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	
	80					85					90					
AAC	ATT	TGC	GAT	GAG	GAC	AGC	GCT	ACA	GAA	ACC	TGC	TAC	TGA			282
Asn	Ile	Cys	Asp	Glu	Asp	Ser	Ala	Thr	Glu	Thr	Cys	Tyr	*			

95

100

105

ATTC

286

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..105

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG GAC AAT CAG	48
Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln	
95 100 105 110	
ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC AGC GCT ACA	96
Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr	
115 120 125	
CTT TGG ACG	105
Leu Trp Thr	

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT	60
T	61

## (2) INFORMATION FOR SEQ ID NO:16:

000518-010998

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGC GCCTCGT GAACGGCAAAA 60  
 ACTGCGGATT CCCGGAAGTA ACACCCTCTC AGTGCCTAA TAAAGGCTGC TGTTTTGATG 120  
 ACACGGTACG GGGCGTTCCG TGGTGCTTCT ACCCCAATAC AATTGACGTT CCGCCTGAAG 180  
 AAGAGTGCGA GCCGTAAG 198

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys  
 1 5 10 15  
 Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu  
 20 25 30  
 Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg  
 35 40 45  
 Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr  
 50 55 60  
 His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu  
 65 70 75 80  
 Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp  
 85 90 95  
 Ser Ala Thr Glu Thr Cys Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr  
 100 105 110  
 Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr  
 115 120 125

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr  
85 90

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Trp Thr  
35

(D) TOPOLOGY: linear

Ala Arg Ile Thr Ser Arg  
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Glu Phe  
65

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 421 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGTCCTTC TACTTGCATA ACAAGACCAA CTGTTGTTCA CGTTCACACG AGCATAATGA 60  
 AGATCTTAGT AGGCATCGAG TCTCCTGGGT TTACTTCTAT ATCAGCTTGC ATTGTAGGCA 120  
 TAGTAGCAGG GTGACTTATT GGCCCTCTTA TAGAGTCTAG GATGTTTCAGG CAACGCGTGT 180  
 GCGAAGCATA TGGTGGACAG TCTAGACACA TTCTTCACAC TAGGTTGTCT CCATCTCGAC 240  
 CTGTTAGTCT ATCAGTGACG CTGAGTTTCG TTGTAAACGC TACTCCTGTC GCGATGTCTT 300  
 TGGACGTCGT GGATGCTATC CTTGTTTACG ATGTGCCGGC ACCAAGGCGA GCACATACCA 360  
 CCTCTCTGTT TTTACCACCT TTGACGGGAA TGCGGGCTAC GTACGATAGG CCTGACTTAA 420  
 G 421

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGTCTTCA CGTTCACACG AGCATAATGA AGATCTTAGT AGGCATCGAG TCTCCTGGGT 60  
 TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA 120  
 TAGAGTCTAG GATGTTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA 180  
 TTCTTCCTAC TCCTGTCGCG ATGTCTTTGG ACGACTTAA 219

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTAGTAGGCA TCGAGTCTCC TGGGTTTACT TCTATATCAG CTTGCATTGT AGGCATAGTA 60

0005310.010999



120

140

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## 31

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 44 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## 60

117

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGTTGTTCA CGTTCACACG AGCATAATGA AGATCTTAGT AGGCATCGAG TCTCCTGGGT	60
TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA	120
TAGAGTCTAG GATGTTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA	180
TTCTTCACAC TAGGTTGTCT CCATCTCGAC CTGTTAGTCT ATCAGTGACG CTGAGTTTCG	240
TTGTAAACGC TACTCCTGTC GCGATGTCTT TGGACGATGA CT	282

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCTGTGTA AGAAGTGTGA TCCAACAGAG GTAGAGCTGG ACAATCAGAT AGTCACTGCG	60
ACTCAAAGCA ACATTTGCGA TGAGGACAGC GCTACACTTT GGACG	105

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

000534.01099  
000000.00000

(2) INFORMATION FOR SEQ ID NO:36:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACTTCGCTAC	TGCTGCTATT	CCGGGTTTGC	CTCTGGACAT	GACAACGCGG	AGCACTTGCC	60
GTTTTGACGC	CTAAGGGCCT	TCATTGTGGG	AGAGTCACGC	GATTATTTCC	GACGACAAAA	120
CTACTGTGCC	ATGCCCCGCA	AGGCACCACG	AAGATGGGGT	TATGTTAACT	GCAAGGCGGA	180
CTTCTTCTCA	CGCTCGGCAT	TCTTAA				206

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Glu Asn Leu Tyr Phe Gln Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Lys Ala His Lys Val Asp Met Val Gln Tyr Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Val Gln Tyr Thr  
1

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Lys Ala Val Ala Asp



Lys Asp Glu Leu  
1

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala Ile Gln Asp Pro Arg Leu Phe Ala Glu Glu Lys Ala Val Ala Asp  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT	60
T	61

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

CTAGAAGTAA TACGAGCACA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC	60
T	61

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

GATCAGAAGT GCAAGTGTGC TCGTATTACT T 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

CTAGAAGTAA TACGAGCACA CTTGCACTTC T 31

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGTCCGC TCGTATTACT 60

T

61

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAGAAGTAA TACGAGCGGA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC 60

T

61

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGGAAG ATGAACGTAT TGTTCTGGTT GACAACAAGT GCAAGGTTGC TCGTATTACT 60

T

61

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTAGAAGTAA TACGAGCAAC CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC 60

T

61

366070" 27E300660



## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAA

47

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATACGGATG TTACGTTCTGA CTATATCTTC ATTTGGGTCC TCTGAGCTAC GGATGATT

58

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGA ATATCTCAG

49

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

000533 010930

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGC ACATCTCAG

49

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACGGACTTGT AGGATCTGAG ATATTCTCCC GGTTATTCAG TGGGACGAT

49

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACGGACTTGT AGGATCTGAG ATGTGCTCCC GGTTATTCAG TGGGACGAT

49

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

03005313 040993  
00000000 00000000

44

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

33

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

60

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

44

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

44

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

60

62.

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

60

62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCTGTGTA AGAAGTCTGA TATCGATGAA GATTCCGCTA CAGAAACCTG CAGCACATG 59

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AATTCATGTG CTGCAGGTTT CTGTAGCGGA ATCTTCATCG ATATCAGACT TCTTACACA 59

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GATCTGTCTA AGAAGTCTGA TATCGATGAA GATTACAGAT TCTTCAGACT ATAGCTACTT 60

CTAA 64

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

000534B-01099B  
B66070-9FE50060

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

64

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

41



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAGCGGAACC ACGGCCGTGT AGCATTTGTT CCTATCGTAG GTGCTGCA

48

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACTG

50

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AATTCAGTCC GGATAGCATG CATCGGGCGT AAGGGCAGTT TCCACCATT TGTCTCTCC

60

ACCATACAC

69

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09005318 040998  
866070 8450060



ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACAA GGATGAATTG	60
TG	62

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

AATTCACAAT TCATCCTTGT CCGGATAGCA TGCATCGGGC GTAAGGGCAG TTTCCACCAT 60  
TTTTGTCTCT CCACCATA CA 81

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

GATCAGGTCG CTGCCATCCA AGACCCGAGG CTGTTCGCCG AAGAGAAGGC CGTCGCTGAC 60

TCCAAGTGCA AGTGTGCTCG TATTACTT 88

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTAGAAGTAA TACGAGCACA CTTGCACTTG GAGTCAGCGA CGGCCTTCTC TTCGGCGAAC 60

AGCCTCGGGT CTTGGATGGC AGCGACCT 88

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGGTACGAAT TCCAGGTSMA RCTGCAGSAG TCRG 34

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ACAGATATCG GGATTTCTCG CAGACTC 27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACAGAATATC GTCAACACCT TCCCACCC 28

(2) INFORMATION FOR SEQ ID NO:87:

0505318 010998

- (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACAAAGCTTT TATTTACCCG ACAGACGGTC

30

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCCCCCCTC GAGCGAYATY SWGMTSACCC ARTCT

35

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACACTGCAGC AGTTGGTGCA GCATCAGC

28

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGCAGGAAG CGGAAGCGGA GGAAGCGGAA GCGGAGGAAG CGGAAGCGAA TTC

53

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CCTTCGCCTT CGCCTCCTTC GCCTTCGCCT CCTTCGCCTT CGCTTAA

47

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ACAGGATCCA TGGAAACCCC AGCGCAGCTT CTCTTCCTCC TGCTACTCTG GCTCCCAAGA

60

TACCACCGGA CCCGGG

76

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

355010"BT50060

TGGTACAGAT CTAGGTSMAR CTGCAGSAGT CRG

33

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ACAGGAATTC AATTTTCTTG TCCACCTT

28

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTCTAGAGA YATYSWGMTS ACCCARTCT

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ACACCGCGGC AGTTGGTGCA GCATCAGC

28

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid

09005318 010998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

(2) INFORMATION FOR SEQ ID NO:98:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

(2) INFORMATION FOR SEQ ID NO:99:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

GCGATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGCGCCTCGT GAACGGCAAA 60  
ACTGCGGATT CCCGGAA 77

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

GTTTTGCCGT TCACGAGGCG CAACAGTACA GGTCTCCGTT TGGGCCTTAT CGTCGTCATC 60  
GCTTCA 66

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

GTAACACCCT CTCAGTGC GC TAATAAAGGC TGCTGTTTTG ATGACACGGT ACGGGGCGTT 60  
CCGTGGTGCT TC 72

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCCCGTACC GTGTCATCAA AACAGCAGCC TTTATTAGCG CACTGAGAGG GTGTTACTTC 60  
CGGGAATCCG CA 72

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TACCCCAATA CAATTGACGT TCCGCCTGAA GAAGAGTGCG AGCCGTAAG 49

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AATTCTTACG GCTCGCACTC TTCTTCAGGC GGCAAGTCAA TTGTATTGGG GTAGAAGCAC 60  
CACGGAAC 68

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

255010-2130050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Pro Leu Gly Ile Ile Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Ile Ile Gly Gly  
1

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val Arg Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asp Ala Gly  
1 5 10 15

Ser Ala Asp Gly Gln Ser Arg Ser Ser Ser Ser Lys Val Leu Phe  
16 20 25 30

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

0005348 040093  
 000070 8750060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr
1				5					10					15
Pro	Ser	Pro	Ser	Cys	Cys	His	Pro	Arg	Leu					
16				20					25					

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Asp	Leu
1				5				

0500343 010993  
06070 830060